

acc #2

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Yale University
2      Carlson, John R.
3      Kim, Hunhyong
4      Clyne, Peter J.
5      Warr, Coral G.
6  <120> TITLE OF INVENTION: Novel Family of Odorant Receptor Genes in Drosophila
7  <130> FILE REFERENCE: 44574-5061-US
8  <140> CURRENT APPLICATION NUMBER: US/09/491,577
9  <141> CURRENT FILING DATE: 2000-01-25
10 <150> EARLIER APPLICATION NUMBER: US 60/117,132
11 <151> EARLIER FILING DATE: 1999-01-25
12 <160> NUMBER OF SEQ ID NOS: 112
13 <170> SOFTWARE: PatentIn Ver. 2.1
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15 <211> LENGTH: 767
16 <212> TYPE: DNA
17 <213> ORGANISM: Drosophila melanogaster
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20 <222> LOCATION: (1)..(765)
21 <223> OTHER INFORMATION: DOR 22A.2, coding region of NCBI Accession No.
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27     cgg gtt aag tcc cga gat gcc ttc gtt tac tta gat cgg gtg atg tgg      96
28     Arg Val Lys Ser Arg Asp Ala Phe Val Tyr Leu Asp Arg Val Met Trp
29             20             25             30
30     tcc ttt ggc tgg aca gtg cct gaa aac aaa agg tgg gat cta cat tac      144
31     Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr
32             35             40             45
33     aaa ctg tgg tca act ttc gtg aca ttg ttg ata ttt atc ctt ctg ccg      192
34     Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro
35         50             55             60
36     ata tcg gta agc gtt gag tat att cag cgg ttc aag acc ttc tcg gcg      240
37     Ile Ser Val Ser Val Glu Tyr Ile Gln Arg Phe Lys Thr Phe Ser Ala
38         65             70             75             80
39     ggt gag ttt ctt agc tca atc cag att ggc gtt aac atg tac gga agc      288
40     Gly Glu Phe Leu Ser Ser Ile Gln Ile Gly Val Asn Met Tyr Gly Ser
41             85             90             95
42     agc ttt aaa agt tat ttg acc atg atg gga tat aag aag aga cag gag      336
43     Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu
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46   Ala Lys Met Ser Leu Asp Glu Leu Asp Lys Arg Cys Val Cys Asp Glu
47           115                      120                      125
48   gag agg acc att gta cat cga cat gtc gcc ctg gga aac ttt tgc tat   432
49   Glu Arg Thr Ile Val His Arg His Val Ala Leu Gly Asn Phe Cys Tyr
50           130                      135                      140
51   att ttc tat cac att gcg tac act agc ttt ttg att tca aac ttt ttg   480
52   Ile Phe Tyr His Ile Ala Tyr Thr Ser Phe Leu Ile Ser Asn Phe Leu
53           145                      150                      155                      160
54   tca ttt ata atg aag aga atc cat gcc tgg cgc atg tac ttt ccc tac   528
55   Ser Phe Ile Met Lys Arg Ile His Ala Trp Arg Met Tyr Phe Pro Tyr
56           165                      170                      175
57   gtc gac ccc gaa aag caa ttt tac atc tct agc atc gcc gaa gtc att   576
58   Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile
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61   Leu Arg Gly Trp Ala Val Phe Met Asp Leu Cys Thr Asp Val Cys Pro
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64   Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln
65           210                      215                      220
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67   Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr
68           225                      230                      235                      240
69   ttg aag gag ctc gcc gac tgc gtt cga gat cac cgc ttg ata ttg ga   767
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74 <212> TYPE: PRT
75 <213> ORGANISM: Drosophila melanogaster
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81   Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr
82           35               40               45
83   Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro
84           50               55               60
85   Ile Ser Val Ser Val Glu Tyr Ile Gln Arg Phe Lys Thr Phe Ser Ala
86           65               70               75               80
87   Gly Glu Phe Leu Ser Ser Ile Gln Ile Gly Val Asn Met Tyr Gly Ser
88           85               90               95
89   Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu
90           100              105              110
91   Ala Lys Met Ser Leu Asp Glu Leu Asp Lys Arg Cys Val Cys Asp Glu
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93   Glu Arg Thr Ile Val His Arg His Val Ala Leu Gly Asn Phe Cys Tyr
94           130              135              140

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98                      165                      170                      175
99      Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile
100                      180                      185                      190
101     Leu Arg Gly Trp Ala Val Phe Met Asp Leu Cys Thr Asp Val Cys Pro
102                      195                      200                      205
103     Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln
104                      210                      215                      220
105     Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr
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123     Pro Arg Ile Ser Gly Leu Ile Val Gly Leu Trp Pro Gln Arg Ile Arg
124         20              25              30
125     ggc ggg ggc ggt cgt cct tgg cac gcc cat ctg ctc ttc gtg ttc gcc      144
126     Gly Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
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130         50              55              60
131     gtc cac ctg gac aac ctg gtg gtg gcg ctg gag gcc ttc tgc ccc gga      240
132     Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
133         65              70              75              80
134     acc acc aag gcg gtc tgc gtt ttg aag ctg tgg gtc ttc ttc cgc tcc      288
135     Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
136         85              90              95
137     aat cgc cgg tgg gcg gag ttg gtc cag cgc ctg cgg gct att ttg ctc      336
138     Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu
139         100             105             110
140     agc ctg ttg ttg ctc agc tct ggc acg gcg aca aat gcc gcc ttc acc      384
141     Ser Leu Leu Leu Leu Ser Ser Gly Thr Ala Thr Asn Ala Ala Phe Thr
142         115             120             125
143     ttg caa ccg ctg att atg ggt ctc tac cgc tgg att gtg cag ctg cca      432
144     Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp Ile Val Gln Leu Pro

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148          145          150          155          160
149      cag cca gga gtc ttt ccg ctc acc tac gtg ctg ctg acc gct tcc ggt 528
150      Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly
151          165          170          175
152      gcc tgc acc gtt ttc gcc ttc agc ttc gtg gac gga ttc ttc att tgc 576
153      Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys
154          180          185          190
155      tcg tgc ctc tac atc tgc ggc gct ttc cgg ctg gtg cag cag gac att 624
156      Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile
157          195          200          205
158      cgc agg ata ttt gcc gat ttg cat ggc gtg gat gtg ttc acc gag gag 672
159      Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu
160          210          215          220
161      atg aac gcg gag gtg cgg cac aga ctg gcc caa gtt gtc gag cgg cac 720
162      Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His
163          225          230          235          240
164      aat gcg att atc gat ttc tgc acg gac cta aca cgc cag ttc acc gtt 768
165      Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val
166          245          250          255
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169          260          265          270
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177      Gly Gly Asn His Val Ser Glu Ser Ser Ala Val Ala Asp Val Leu
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186      Phe Phe Thr Pro Ser Leu Pro Ala Leu Arg Ser Ile Leu Ser Thr Ala
187          355          360          365
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192 <211> LENGTH: 379
193 <212> TYPE: PRT
194 <213> ORGANISM: Drosophila melanogaster

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201 35 40 45
202 Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
203 50 55 60
204 Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
205 65 70 75 80
206 Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
207 85 90 95
208 Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu
209 100 105 110
210 Ser Leu Leu Leu Ser Ser Gly Thr Ala Thr Asn Ala Ala Phe Thr
211 115 120 125
212 Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp Ile Val Gln Leu Pro
213 130 135 140
214 Gly Gln Thr Glu Leu Pro Phe Asn Ile Ile Leu Pro Ser Phe Ala Val
215 145 150 155 160
216 Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly
217 165 170 175
218 Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys
219 180 185 190
220 Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile
221 195 200 205
222 Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu
223 210 215 220
224 Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His
225 225 230 235 240
226 Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val
227 245 250 255
228 Ile Val Leu Met His Phe Leu Ser Ala Ala Phe Val Leu Cys Ser Thr
229 260 265 270
230 Ile Leu Asp Ile Met Leu Asn Thr Ser Ser Leu Ser Gly Leu Thr Tyr
231 275 280 285
232 Ile Cys Tyr Ile Ile Ala Ala Leu Thr Gln Leu Phe Leu Tyr Cys Phe
233 290 295 300
234 Gly Gly Asn His Val Ser Glu Ser Ser Ala Ala Val Ala Asp Val Leu
235 305 310 315 320
236 Tyr Asp Met Glu Trp Tyr Lys Cys Asp Ala Arg Thr Arg Lys Val Ile
237 325 330 335
238 Leu Met Ile Leu Arg Arg Ser Gln Arg Ala Lys Thr Ile Ala Val Pro
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VERIFICATION SUMMARY
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